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RESULT
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                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0243 row: K column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10243K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0243K14 R, DNA sequence.
                                                                                                                                          Seq primer: CACACAGGAAACAGCTATGACCCClass: plasmid ends
                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         High quality sequence stop: 684
                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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/clone_lib="prosBAC"
/clone="BACN37F07"
/note="end : SP6"
a 70 c 85 g
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="Texon:10090"
/clone="UUGC1M024JK14"
/clone_lib="Mouse 10kb plasmid
                                                                                                       ocation/Qualifiers
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                                                                                                           2 (bases 1 to 524)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bound
Bernot,A., Fizames,C., Wincker,P., Brottler,P.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL167541.1 GI:7805598
GSS; genome survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 196C24 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                               Bouneau, L., Billault, A., Quetier, F., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acaathomorpha; Acaathopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis. Tetraodon nigroviridis
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                                                               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H.,
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                                         Unpublished
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                   (bases 1 to 524)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
125 c 123 g 238 t
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                                                                                                                                                                                                                                                                                                                                                                          Tetraodon.
                                                                                                                                                                                                                                                                                                Jaillon,O., Dasilva,C., Fizames,C., lt,A., Quetier,F., Saurin,W., Bernot,
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Pred. No. 9
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                                                                                                                                      Quetier, F.,
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                                                                                                                            Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Taqawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB795590
BB795590
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                  Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                          Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
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    Suehiro-cho,
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/clone_1ib="G"
/note="Genoscope sequence
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/db_xref="taxon:99883"
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Pred. No. 17;
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Yokohama, Kanagawa
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                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1064)

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila

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Drosophila melanogaster genome sum
BACR04C22 of RPCI-98 library from
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                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.f)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                           Direct Submission
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Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                            fruit fly.
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further details.
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64; Conservative
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/ceil_type="stroma cell"
/ceil_line="CRL-2028 SR-4987"
/cell_line="CRL-2028 SR 224 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="G431005L12"
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Pred. No. 26;
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carried out as part of Genome Project (BDGP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.6%;
al Similarity 42.4%;
115; Conservation
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further informat
                                                                                                                                                                                                                                                                                                                                                                                               GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genos
                                                                                                                                                                             Genoscope.
Direct Submission
                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence. AL069257 GI:4949400
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR04C22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the content of the co
                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. | Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., E., Kohn,S., Shn,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
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correct orientation)
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
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Mus musculus
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77; Conserv
                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:7227"
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                                                                                                                                                                           AUTHORS
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               Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as pari
Collaboration with the European Drosophila Genome Project (EDC
http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence T7 end of EBACN14J12 of DrosBAC library from Drosophila melanogaster
                                                                                                                                                                                         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 739)
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                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E:mail : seqref@genoscope.cns.fr
                                                                                                                                                                         Genoscope.
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/clone="IMAGE:598508"
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                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        project grant. The DNA was prepared from embryos by and Genevieve Payan. It has been constructed in the
                                                                                           Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other_GSSs: RPCI-24-294M13.TV
                                                                                                                                                                                                                                                                                                                                  Zhao.S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeor Russell,D., de Jong,P. and Fraser,C.M.
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                                             page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 294 row: M column: 13
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/organism="Mus musculus"

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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; The Indian Condition of the John Condition of the J
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length: 0 length: 2000000000

Total number Searched:

of hits satisfying chosen parameters:

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1797656 seqs, 10463268293 residues

Scoring table: Perfect score: Sequence:

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GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen Ltd

Post-processing: Minimum Match 0%
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_htg_other:*
em_htgo_inv:* em_htg_hum: *
em_htg_inv: *

SUMMARIES

Result. Score Query Match Length DB ij

Description

JOURNAL MEDLINE REFERENCE AUTHORS REFERENCE AUTHORS SOURCE ORGANISM KEYWORDS TITLE Carybdea rastonii Eukaryota; Metazoa; Cnidaria; Cubozoa; Cubomedusae; Carybdeidae; Carybdea rastoni cDNA to mRNA. Carybdea toxin-1

cds.

INV 06-SEP-2000

JOURNAL TITLE Novel proteinaceous toxins from the box jellyfish (Sea wasp) carybdea rastoni blochem. Blophys. Res. Commun. 275 (2), 582-588 (2000) Nagai,H., ' 0422301

2 (bases 1 to 1630)
Nagai, H. and Takuwa, K.
Direct Submission
Submitted (29-JUN-1998) Hiroshi Nagai, Suntory Institute for
Bioorganic Research; Wakayamadai 1-1-1, Shimamoto, Osaka 618-8503,

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                           AAGGTAGAAACTGCCTTAAAAGAAGCTTCTGGTAGCAACGAGGCTGCTCTTGAGGCTTTA
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Fax:81-75-962-2115).
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/db_xref="01:9988402"
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LHKLIPEGALIGAVYHPISASETSKAILNYTKYEGVPDVPRPJGNRRYKFTNSYWNTV
SICSEAYMGNYMFRGCSNVRNPNIRVSKMSDGFYTMENSDRRKLYITKHDQGWGWGTL
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CCGTCATCACCTTCGTCAACAGTGTATCAAAGACAGAGAATCTGACCGAGGTCCATTTGG
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Direct Submission

Submitted (07-JAN-2000) Hiroshi Nagai, Sunto

Bioorganic Research; 1-1-1 Wakayamadai, Shii

618-8503, Japan (E-mail:nagai@sunbor.or.jp,

Fax:81-75-962-2115)
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hawaiian box jellyfish (Sea wasp) carybdea alata
Blochem. Biophys. Res. Commun. 275 (2), 589-594 (2000)
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GQLNDLGTDTKELKEALQGVQEAVKKEPATTIAKVSTIYGSVGGSLSKFKSGDPFDVA
SGCLDIIASVA7TFGGPYGIATGAVASLISSLISLFSGNSMGSAIKQVIDAFKKYBA
QELEDNVKGAKRTFNAVITFVNSVSKTENLTEVHLDSVRDAVRVDAFTNNLGVLESRI
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REFERENCE

FEATURES AUTHORS TITLE JOURNAL

1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkn
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers

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SOURCE KEYWORDS VERSION

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Chiropsalmus quadrigatus
AB045319
AB045319.1 GI:18146992
                                                                                                                                                                                            Submitted (29-JUN-2000) Hiroshi Nagai, Tokyo University of Fisheries; 4-5-7, Konan, Minato-ku, Tokyo 108-8477, Japan (E-mail:nagai@tokyo-u-fish.ac.jp, Tel:+81-3-5463-0454,
                                                                                                                                                                                                                                                                                                                                                                               Chiropsalmus
Chiropsalmus
                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                 Nagai, H
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Biosci. Biotechnol. Biochem. 66, 97-102 (2002)
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synthetic construct
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sk,A., Piepenbrock,C. and Berlin,K.
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EYAVSKAFLDGVRNETSDLSPTGVSALGANDPVQGDVRRIAMVQRIKNKKPRTESEI
KRVLSMLELFTDLCSLRDLILLDLYQLVATPGHSPNIASGIKEVSNLGREEYKKVFED
LLKTNDKETYLFLSYLVPRERNEQSQKIFKFFDLMKVKYDDRLKQDLTGLQVFSSLHW
PNYFLCSSKDYLALICTKPYGSLRLDKLNDGFYSIKTTQSNPKVCHRYGEYILFTHDR
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genom
1002 c 12377 g 27036 t
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Local Similarity 47.6%;
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             aggatatgtttgaaagaaacaaaaaaaaaaa 1610
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                                            AAACCCAAAACCCTAAACGTTACTAAA----ATACTTTTATTAATAATAATAATAATATCCCT 3612
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//db_xxef="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
247 c 2903 g 8189 t
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Pred. No. 1.1;
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Sequence 22 from Patent W00111061.
AX083744
                                                                                                          Kunst,L. and Clemens,S.
Regulation of embryonic transcription
Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
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/db_xref="taxon:32630"
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
93 c 1898 g 4787 t
                                  /note="consensus sequence of A.t.,
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 ctaatttcatattaaacattaatgtttccttataatgcatttt 1551
                                                                                                                                                                                          tcgcagctgggaaaataatccaggacctcaaggacattggagtataacataattaaagag
                                                                                                                                                                                                                                                         aagctctaagaggtggcccaactggttcatgtatatggaatcaagtgccagtggctacat
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                                  YAYMHHMHKKGKAAWTNNKTABRDDHBAHVKTYWYWRYDYWCAMCWMNAKAKVRTAMKHM
                                                             gtgcacacttgtatttctacataggatgtcgtcatgaaagtccataaaccatccagcgga
                                                                                                                                                              NNKAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRRABHR
                                                                                                                                                                                                                                                                                          NNBKAMYMRVAWMMYSRDTTNTDWMMWTSDWBWHWYTVDYTMMRAWNNNNNNWRBCKTT
                                                                                                                                                                                                                                                                                                                                                      WTYWMGNNTMWMRRAWKMMNMAWCRRAYCCNNNNNRACVWHKHKMWRWTWKYMWKAACNN 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNSCCTCTRMMTMRWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWYANWMRCRDVTY
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                                                                                                                                                                                                                           SWMWWMDHMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMGKTMTNNNN
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tive 377;
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                    gcatacgaatataagacatcaaacgaatgcagtacttaaagt 1450
                                                                                                      caggacctcaaggacattggagtataacataattaaagaggaatcaacaatgtcccaaag
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                                                             TATAATATCAATTGAAGAGTTTGATAGTATAATTCCTGTTAAGCCCCCCAAGGGTAAAAAG
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoca
Aculeata; Apoidea; Halictidae; Halictinae; Halictini;
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/protein_id="AAF14165.1"
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/db_xref="G1:6492072"
/t-anslation="RANVSFWILLIPALSSILSSSIYSTGTGTGWTVYPPLSSIMFHS
SNSVDFTIFSLHIAGISSIMGAINFIVSIMLMKNISLNFDQIPLFPWSVSITAIILLL
SLPYLAGAITMLLTDRNLNTSFFDPSGGGDPILYQHLFWFFGHPEVYILILPGFGLIS
SLPYLAGAITMLLTDRNLNTSFFDPSGGGDPILYQHLFWFFGHPEVYILILPGFGLIS
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FLGLMGMPRRYSDYPDAYYCWNIISSIGSLISFNSMILLIYIMLESLISKRMVMFKYS
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/db_xref="taxon:88531"
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                                                                            Olek, A., Piepenbrock, C. and Berlin, K. Method and nucleic acids for the analysis Patent: WO 0202808-A 1 10-JAN-2002;
                                                                                                                                                                                                7001 bp
Sequence 1 from Patent W00202808
AX349075
                                                                                                                                             synthetic construct
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AX347354
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Method and nucleic acids for the differentiation of astrocytoma oligoastrocytoma and oligodendroglioma tumor cells Patent: WO 0200705-A 1 03-JAN-2002;
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ilarity 47.4%;
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/db_xxef="taxon:32630"
/note="chemically treated genomic 40 c 1249 g 3403 t
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 /note="chemically treated genomic
               /organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic construct synthetic construct
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/db_xref="taxon:32630"
/note="chemically treated genom
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                                                                                                                                                                                                                                                                                                            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 174,019 genomic DNA of 21921.1-921.2 Published Only in DataBase (2000) In press 2 (bases 1 to 174019)
    Homo sapiens genomic DNA, chromosome AP001674 AL163219 BA000005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B853K11, LL56-APP region, complete sequence.
                                            AP001674
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On May 30, 2000 this sequence version replaced gi:7717271.
The Chromosome 21 mapping and sequencing consortium consisting of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         see below)
                                                                                                                                                                                                                                                                                                        * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Bra
info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                                                160-8582, Japan,
* e.mail: nshimizu@dmb-med.keio.ac.jp/
* URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yaspo,M.L
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                                                                                                                                                             Max-Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany, e.mail: info-chr21@molgen.mpg.de URL: http://chr21.rz-berlin.mpg.de/L163219: Submitted (10-Apr-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.mail: hattori@gsc.riken.go.jp
URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                     URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL: http://genome.imb-jena.de,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (sites)
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∕organism="Homo sapiens"
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/chromosome="21"
                                                                                                                                          Location/Qualifiers
                     note="Accession No. AP001537"
                                                                                                                           340000
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Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M. and Schudy,A. The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium Nature 405 (6784), 311-319 (2000)
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Hattori,M., Fujlyama,Å., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishi,K., Totokk,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschnidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barandt,P., Scharfe,M., Schoer,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Bek,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and

Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses

* RIKEN Genomic Sciences Center, Human Genome Research Group, Sagamihara 228-8555, Japan,

* Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de

Keio University School of Medicine, Molecular Biology, * Tokyo

Braunschweig, Germany,

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11 BAC library"
     rpt_family="Simple_repeat"
rpt_type=TANDEM
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rpt_type=DISPERSED
8847. .19585
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note="MER53"
rn+ f-
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'rpt_family="LINE/L1"
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'clone_lib="RPCI-11 BAC library"
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                                                                                          rpt_family="Simple_repeat"
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1. .8370
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_type=DISPERSED
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5. .19917
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Best Local Similarity
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                                  59614 CATGTATCAAAACATACATATTTATGTATATATCATAACTATATAAAATTTCCTTTTTCA 59555
                                                                                                                                                                                 59734 GTATTGTGTATTTAAAGATTGCTCATAGTAGATCTCAAATGTTCTCATTACAAAAATAAA 59675
                                                                                                                                                  1453
                                                                                                                                                                                                        1393 caacaatgtcccaaaggcatacgaatataagacatcaaacgaatgcagtacttaaagtgc 1452
                                                                                                                                                                                                                                                                                          1333 agctgggaaaataatccaggacctcaaggacattggagtataacataattaaagaggaat 1392
1573 tttcaagaggatatgtttgaaagaaacaaaaaaaaa 1610
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                                                                                                         ATGATAGTTGTCAGGTACTAAATATGCTAACTAGCTTGATTTCACCATACCATAATATAAA 59615
                                                                                                                                          acacttgtatttctacataggatgtcgtcatgaaagtccataaaccatccagcggactaa 1512
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/note="(TA)n"
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/note="AluSx"
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Pred. No. 6.4;
D; Mismatches 147;
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Length 340000; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 19, 2000 this sequence version replaced gi:7329419. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1995-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCarthy, M., McEwan, P., McGurk, A., McKernan, R., McPheeters, R., Weldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vola, Milson, B., Will, N., Wyman, D., Ye, W.J., Vola, R., Viel, R., Vola, M., Wilson, B., Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young,G., Zainoun,J., Zimmer,A. and Zody,M. Direct Submission
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Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                     Sequencing vector: M13; M79815; 100% of reads
Sequencing vector: M13; M79815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 184383 bases at least 040
Consensus quality: 184383 bases at least 030
Consensus quality: 193096 bases at least 020
Insert size: 170000; agarose-fp
Insert size: 194121; sum-of-contigs
Quality coverage: 4.6 in 020 bases; agarose-fp
Quality coverage: 4.0 in 020 bases; sum-of-contigs
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SEQUENCE, 17 unordered pieces
NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 599_J_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
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73270 73369: gap of 100 bp
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21413 21512: gap of 100 bp
21513 27609: contig of 6097 b
27610 27709: gap of 100 to
17710 32804
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73370, .89506
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195721: cont
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122927: cont:
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22: gap of 100 bp
10464: contig of 3802 bp in length
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32894: contig of 5185 bp in length
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6562: contig of 4810 bp in length
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ORIGIN
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Search completed: June 12, 2002, 18:00:40 Job time: 59091 sec

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Result
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Maximum DB
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                                                                                                                                                                                                                                               Score
1610
277
46.2
43.8
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length: 2000000000
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Listing first 45 summaries
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2: \SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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Tumour suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. rastonii hemolytic protein DNA.
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ALIGNMENTS

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                                                                                            agaaatatcgcgatcaagagttggaagacaatgtaaaaggagcaaaaaggacctttaatg
                                                                                                                                    gcctcttctctggaaatagtatgggaagtgcaatcaaacaagttattgacgacgctttca
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54.1%;
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Human; tumour suppressor gene; oncogene; antitumour; cancer; tumour; CpG dinucleotide; single-nucleotide |
                                                                                                                         AAS46794;
                                                                                                                                                       AAS46794 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated MIA, (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (ss) and sequences complementary to (ss). The nucleic acid may be a CC peptide nucleic acid oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CPG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC cancers and tumours. The probes can also be used in a method for CC cancers and stating diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diseases is to parameters one of the CC companes Scarulp as basis for diseases to sequence is one of the CC sared search and contained and contained sequences derived from tumour suppressor genes and CC concerns "Concerns Contained and contained con
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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01-SEP-2000;
  1602 aaaaa 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                     agacatcaaacgaatgcagtacttaaagtgcacacttgtatttctacataggatgtcgtc
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                                           TATAAATTCACATAAAATAAAAACTTAAACTATTAATATATATATATAAACTAAACG
                                                                                                                                                                            atgaaagtccataaaccatccagcggactaatttcatattaaacattaatgtttccttat
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                                                                                                                                                                                                                                                                                                                   128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46.2; DB 22; Pred. No. 0.073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 56153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                           1400
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                                                                                                                                                                                                                    Sequence 15548
                                                                                                                                                                                                                                                                                                                            genes which
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                       macular
                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL34155
                                                                                                                                                                                                                                                         macular degeneration, arteriosclerosis, anaemia, cancer, acute mye
leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                         leic acid comprising fragment of chemically modified diagnosis and treatment of diseases associated with
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2002-130909/17
                                                                 gtcccaaaggcatacgaatataagacatcaaacgaatgcagtacttaaagtgcacacttg 1459
                                                  129;
                     tatttctacataggatgtcgtcatgaaagtccataaaccatccagcggactaatttcata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune system disease; cytosine methylation;
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
                                                                                                                                                                                                                                             The present sequence is a gene of the invention
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                      BP; 4209 A;
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                                                                                                                                                                 2.7%;
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                                                                                                                                                                                                                                                                                                                                                                32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin
                                                                                                                                                                                                                      247 C;
                                                                                                                                                     Score 43.8; DB Pred. No. 0.19; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                      2903 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                              DВ
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                                                                                                                                                      142;
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                                                                                                                                                                                                                      0 other;
                                                                                                                                                      Indels
                                                                                                                                                                             Length 15548
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abnormal
                                                                                                                                                                                                                                                                                    acute myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                     useful
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ABL32682/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11647
                                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                              Sequence 9733 BP;
                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute myeloid leuk neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL32682 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory;
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                                                                                                         Local Similarity
cgaatgcagtacttaaagtgcacacttgtatttctacataggatgtcgtcatgaaagtcc 1491
                                                          ataacataattaaagaggaatcaacaatgtcccaaaggcatacgaatataagacatcaaa 1431
                                        2002-130909/17
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                                                                                                                                                                                                                                                                                                          1; SEQ ID NO 655;
                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia; Alzheimer's disease; AIDS; epilepsy; sis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                                              2955 A; 93 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                         2.7%;
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                                                                                                                                                                                                                                                                                                       32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin
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                                                                                                         Score 43.2;
Pred. No. 0.
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                                                                                             Mismatches
                                                                                                                                                              1898 G;
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                                                                                                                                                            4787 T;
                                                                                                         . 22;
                                                                                             113;
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                                                                                                                                                          0 other;
                                                                                                                    Length
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                                                                                           Gaps
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В δÃ

Sequence 7302 BP.;

1703 A; 147 C; 1814 G;

3638 T;

0 other;

Local Similarity

Conservative

2.7%;

Score 42.8; DB Pred. No. 0.25; Mismatches

Length

142; 24;

0

1340 aaaataatccaggacctcaaggacattggagtataacataattaaagaggaatcaacaat 1399

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RESULT 6
ABL32711/c
 \begin{array}{l} \mathbf{X} \times \mathbf{C} \times \mathbf
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                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, eppliepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; eye disease; arterioscierosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fractor diagnosis and treatment
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01-SEP-2000;
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antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 684; 32pp + Sequence Listing; German
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2000DE-1043826
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AAS46746/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2000;
30-JUN-2000;
01-SEP-2000;
numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oilgomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation st and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the
                                                                                                                                                                                                                                                                                           genes and analysing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6715
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                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence bases, of a segment of chemically pretreated DNA (CP DNA) e.g bisulphite, of genes associated with tumour suppression and oncogenes having a segmence taken from 536 (actually 533 since
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1400
                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                  Olek
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06-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS46746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS46746 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTCATAAAAACTAAAATTAAATAAATAAAATAATATTTCATAAAAACACGATTTC
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                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                                                                        SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock
                                                                                                                                                                                                                                                                                             of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-EP02955.
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2000DE-1032529
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2000DE-1019058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000DE-1043826
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                                                                                                                                                                                                                                                     27pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemically modified sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphism;
                                                                                                                                                                                                   ence of 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electro format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary sequence ID 2 and ID1, ID 536 is missing).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1372 ataacataattaaagaggaatcaacaatgtcccaaaggcatacgaatataagacatcaaa 1431
                                                                                                                                            SNOM)
                                                                                                                                                                                                                                            WO200151627-A2
                                                                                                                                                                                                                                                                   Glycine
                                                                                                                                                                                                                                                                                                                 Soybean; antihelmintic;
                                                                                                                                                                                                                                                                                                                                         Soybean 515002 region G2,
                                                                                                                                                                                                                                                                                                                                                                                           AAI61370;
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                                                                    New purified
                                                                                           WPI; 2001-425872/45
                                                                                                                                                                    07-JAN-2000; 2000US-0174880
                                                                                                                                                                                            05-JAN-2001; 2001WO-US00552
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                                                                                                                                                                                                                                                                                                      resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgaatgcagtacttaaagtgcacacttgtatttctacataggatgtcgtcatgaaagtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115;
                                                                                                                                                                                                                                                                                         region G3;
                                                                                                                                                                                                                                                                    max
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                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38342 BP; 12471 A;
                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                    nucleic acid for
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                          resistance
                                                                                                                                                                                                                                                                                        lmintic; gene therapy; soybean cyst
  rhg1; Rhg4; SCN resistant allele;
3; 318013 region A3; 515002 region
                                                                                                                 MĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ce of the corresponding odd numbered sequent and ID 535, except for those whose partner
                                                                                                                   Parsons
                                                                                                                                                                                                                                                                                                                                                                                                                 127197
                                                        and
                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 C;
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                                                       r producing for use in
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                                                                                                                   Parnell LD
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                                                                                                                                                                                                                                                                                                                                         <u>-</u>
                                                      a soybean plant having soybean plant breeding programs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123;
                                                                                                                                                                                                                                                                                                                 cyst nematode;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                           ds
                                                                                                                                                                                                                                                                                                     breeding;
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The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN

Page 131-204;

1353pp;

English

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RESULT 9
ABL32347/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine
      Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                              antiinflammatory, cancer; eye disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsv. neurofibromatosis; rheumatoid arthriti-
                                                WPI; 2002-130909/17
                                                                                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                              03-JAN-2002
                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                  neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecules.
                                                                                                    (EPIG-)
                                                                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32347
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methylation
                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127197
                                                                                                                            2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                        system associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5216
                                                                          Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.2; D
Pred. No. 2.9;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 320
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                                                                                                                                                                                                                                                                                  bowel disease,
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        gene, useful
abnormal
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RESULT 10
ABL34459/c
ID ABL344
XX ABL344
XX BL344
XX Human
DT 26-MAR
DT 26-MAR
XX Metast
KW Cytosi
XX MO2001
XX Homo s
PF 06-APF
PF 06-APF
PF 07-APF
PR 07-APF
PR 01-SEI
XX GPIG-
XX UPI;
XX PT New n:
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryvulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                    06-APR-2001;
                                                                                                                                                                                                                                                                             Human metastasis associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2001.
                                                                                                                                                                                               WO200177376-A2
                                                                                                                                                                                                                                          Metastasis associated gene; cytosine methylation; gene;
                                                                                                                                                                                                                                                                                                                            ABL34459
                                                                                                                                                                                                                                                                                                                                                  ABL34459 standard;
                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5216 BP; 1332 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                        2002-010922/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttaaacattaatgtttcottataatgcattttcatgaaatctctattgtgacatttcaag
                                                                                                                                                                                                                                                                                                                                                                                                         AATATCTAAATTAAAATAAAAAATTATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                              aggatatgtttgaaagaaacaaaaaaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatttctacataggatgtcgtcatgaaagtccataaaccatccagcggactaatttcata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtcccaaaggcatacgaatataagacatcaaacgaatgcagtacttaaagtgcacacttg 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                          ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                                                                                                 2001WO-EP03970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                             Berlin
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                                                                                                                                                                                                                                          cytostatic; gene therapy; cancer; ds.
                                                                                                                                                                                                                                                                            gene SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                  ВP
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Pred. No. 0.
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nucleic acid derived

from

chemically treated

metastasis

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RESULT 11
ABL32805/c
ID ABL328
XX ABL328
AC AB
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Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for also for tr
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     WPI; 2002-130909/17
                                                Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anacute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy neurofibromatosis; rheumatoid arthritis; psoriasis; bowel di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4785
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                                                                                                                                               30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32805
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                                                                                                 (EPIG-)
                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of human metastasis associated es which are modified by cytosine methylation. The sequences can be d in the diagnosis and treatment of cancer. The present sequence is of the genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggatatgtttgaaagaaacaacaaaaaaa
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                                                Piepenbrock
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                                                                                                                                               2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antianaemic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7113
                                                Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                       epilepsy;
bowel disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia;
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В Qγ В Š

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Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation .
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Claim 1; SEQ ID NO 778; 32pp + Sequence Listing; German

including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo: leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. can be used The present which in the diagnosis and treatment of immune system invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences $% \left(1\right) =\left\{ 1\right\} =$ acute myeloid disorders,

Sequence 7113 BP; 1789 A; 245 C; 1791 G; 3288 T; 0 other;

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Best Local
                                            4082
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                                                                                                                                   4202
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                      1552
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                                                                 1492
                ataacataattaaagaggaatcaacaatgtcccaaaggcatacgaatataagacatcaaa 1431
ataaaccatccagcggactaatttcatattaaacattaatgtttccttataatgcatttt 1551
                                                                                     cgaatgcagtacttaaaagtgcacacttgtatttctacataggatgtcgtcatgaaagtcc
                                                                                                                                AAAAATTAAAACTACAATAAACCATAATTATACCACTACACTCCAACCTAAATAACAAAA 4143
                                           115;
                                                                                                                                                                                         Similarity
                                                                                                                                                                              Conservative
                                                                                                                                                                                       2.5%;
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                                                                                                                                                                                      Score 40.6;
Pred. No. 1;
                                                                                                                                                                              Mismatches
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ABL33751/c
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   Olek A,
                          (EPIG-) EPIGENOMICS
                                                                                  02-JUL-2001; 2001WO-EP07537
                                                                                                                               WO200200928-A2
                                                                                                                                                                             gene;
                                                                                                                                                                                        neurofibromatosis;
                                                                                                                                                                                                                                                                                   Human immune
                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                 ABL33751;
                                                                                                                                                                                                                                                                                                                                                       ABL33751 standard; DNA;
                                                30-JUN-2000;
01-SEP-2000;
                                                                                                          03-JAN-2002
                                                                                                                                                      Homo sapiens
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   Piepenbrock
                                               2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                  system
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                                                                                                                                                                                         rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                   associated
                                                                                                                                                                                                                                                                                                         entry)
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   Berlin
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                                                                                                                                                                                        psoriasis; bowel
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disease;

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RESULT 13
AAS453
XX AAS453
XX AAS453
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XX CAL1 C
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XX CAL1 C
XX Human
KW Graft
KW Human
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryvulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                            human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS45324 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1596
                                                                                                                               15-MAR-2001;
                                                                                                                                                                                                        WO200168911-A2
                                                                                                                                                                                                                                                                                                                                                                                                          Chemically pretreated genomic DNA associated with cell cycle #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7037 BP; 2070 A; 134 C; 1475 G; 3358 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1724; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                              immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                             Cell cycle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
               2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                       human; CpG dinucleotide; cytosine methylation; HIV;
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                                                                                                                                 2001WO-EP02945
                                                                                          2000DE-1013847
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                                                                                                                                                                                                                                                                                                  antitumour;
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Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                  cytostatic;
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associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing
                                                                                                                                                                                                                                                                                                                                                                                                                          Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arterioscherosis comprising fragments of chemically modified genes associated with cell cycle
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-)
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  7195
                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID No 29;
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  B₽;
2059 A; 224 C; 1725 G; 3187 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                28pp; English
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Matches 97
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aaccatccagcggactaatttcatattaaacattaatgtttccttataatgcattttcat 1554
                                                                                                               97; Conser
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Pred. No. 1
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RESULT 14
AAX99504/C
ID AAX995
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XX O5-AUC
XX W09339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ureaplasma urealyticum; nucleic acid detection; infe human urogenital tract; pregnancy; neonatal disease; suppurative arthritis; ss.
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                                                                                                                                                                                                                                                                                                       05-AUG-1999
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30-JAN-1998; 29-JAN-1999;

98US-0073189 99WO-US01972

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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Best Local S
Matches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Ureaplasma urealyticum infection. It provides novel genes (AxX99501-681) that can be used as a source of primers and probes for the detection and/ or quantification of U. urealyticum in a biological sample. The probes that can be used in the method of the invention by forming target:probe complex is copmplementary to a region selected from one of the 181 nucleic acid sequences (AAX99501-681). U. urealyticum is an opportunistic pathogen of the human urogenital tract that is a significant cause of adverse pregnancy outcome, neonatal disease, and suppurative arthritis. As the infections are commonly asymptomatic, it is important to have specific and sensitive methods for detecting their presence in a patient. Also, as the pathogen has no current antibiotic directed specifically against it, it would be advantageous to isolate and detect gene sequences which are unique to it, and utilise these as a basis for diagnosis of U. urealyticum infection as well as to develop new and immore a form the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1581
                                                                                                                                                colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS61251 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides methods for the detection of Ureaplasma urealyticum infection. It provides novel go
                      18-OCT-2001
                                                                  WO200177375-A2
                                                                                                                                                                                                                                                  cardiac damage; inflammatory response; asthma: HDR syndrome; congenital heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                Human; Gene regulation-associated gene;
                                                                                                                                                                                                                                                                                                                                            Human gene regulation-associated gene oligonucleotide #206
                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS61251;
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                                                                                                                                                                                                                         renal disease; Preeclampsia; cardiac allograft vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 GAATTAATTTGTGATAAAACATTATAAATA
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 10048
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Pred.
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No. 1;
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                                                                                                                                                                                                                                                  Haemophilia; Werner syndrome; defect; Saethre-Chotzen syndr
                                                                                                                                                                                                                                                                                              severe combined immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
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                                                                                                                                                                                                                                               syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   is bases of a chemically pretreated gene associated with gene regulation conselected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the cytosition to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by associated with gene regulation and in therapy of such diseases, by canabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
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AAAATAAAAAAAAAAAATCACTAAAA
                                  atgtttgaaagaaacaaaaaaaaaa 1610
                                                                        CCCTAAATTTTAATAAAAATAAACTACTAAAAAATTTTACTATAAAATTAAAAT
                                                                                                     cattaatgtttccttataatgcattttcatgaaatctctattgtgacatttcaagaggat 1584
                                                                                                                                             ctacataggatgtcgtcatgaaagtccataaaccatccagcggactaatttcatattaaa 1524
                                                                                                                                                                                                                   AAAAAAACCCTAATTTAATAAAAATAACTACTAAAAAATTTATACATTACAATAAACCTA 3063
                                                                                                                                                                                                                                                                                                102;
                                                                                                                                                                                                                                                                                                               Similarity
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to 224 nucleic acid sequences comprising at least chemically pretreated gene associated with gene regulation
                                                                                                                                                                                                                                                                                                               2.5%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina//BE_COMB.seq:*
/cgn2_6/ptodata/2/ina//BE_COMB.seq:*
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US-08-952-089A-26
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US-08-920-422-17
US-08-920-422-17
US-08-920-423-19
US-08-920-423-3
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US-09-030-607-207
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US-09-030-030-313-207
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US-09-188-930-27
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US-09-247-095-17

US-08-095-737-1

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Sequence 1, Appli
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Sequence 202, Appli
Sequence 101, App
Sequence 3, Appli
Sequence 26, Appli
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Sequence 2, Appli
Sequence 17, Appl
Sequence 17, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                               TOPOLOGY: linear
: IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
US-08-232-463-14
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Patent No. 5670367
                                                                                                                                                                 APPLICATION NUMBER: EP 91 114 300.6 FILLING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEPHONE: (703)833-4109 TELEX: 899149
                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                          TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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US-08-659-188-24

US-08-655-227-24

US-08-655-227-24

US-09-398-326-24

US-07-781-355-1

US-08-923-536A-1

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Best Local Similarity
Matches 21; Conserv
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR TON NUMBER: JP 43361/1992
APPLICATION NUMBER: JP 43361/1992
APPLICATION NUMBER: JP 43361/1992
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                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,284A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1331
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                                                                                                         FILING DATE: 01-MAR-1993
ATTORNEY_AGENT INFORMATION:
NAME: WHITE JR., PAUL E.
REGISTRATION NUMBER: 32,0
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS TITLE OF INVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAKAI, YASUYO
APPLICANT: TANI, YOSHIKI
APPLICANT: SHIBANO, YUJI
APPLICANT: KONDO, HIROTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D
                                                                                           REGISTRATION NUMBER: 32,011
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-3918
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                                 TELEFAX:
                                                    TELEPHONE:
                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%; Score 48.6; DB 1; ilarity 5.8%; Pred. No. 0.00016; Conservative 192; Mismatches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUSHMAN DARBY & CUSHMAN, L.L.P.
                                   (202) 861-3000
)2) 822-0944
                                                                                                                                                                  UMBER: US 08/025,416
01-MAR-1993
ID NO:
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                                                                                           217755/FPS38209US
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; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W. APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
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TOPOLOGY: un
MOLECULE TYPE:
                                                                                                                                                                                                                                                            1137 ggagaatagcgatcggaggaagttgtatatcaccaagcatgaccaaggatggggatgggg 1196
                                 1317 cagtggctacattcgcagctgggaaaataatccaggacctcaaggacattggagtataac 1376
                                                                                                                                                                                            1197 tactttggatgaggatccaggtgaccaaggccatatgaggttcattcctttgagacatgg 1256
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                                                                                                               1257 gaagtatatggtaagctctaagaggtggcccaactggttcatgtatatggaatcaagtgc 1316
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183 rnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrcrargrcrurgrcrgrurararc
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                                                                                                                                                                                                                                                                                                                                       y Match 2.2%; Score 35; DB Local Similarity 9.1%; Pred. No. 0.36;
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                                                                                                                                                           rnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrs
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US-08-095-737-1/c; Sequence 1, Application US/08095737; Patent No. 5487979
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NAME/KEY: misc_feature

; LOCATION: (1)...(289)

; OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEC 150 NOC. 238-01-14
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LENGTH: 289
TYPE: RNA
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                                             GENERAL INFORMATION:
APPLICANT: Diffor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
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        CANT: Fazioli, OF INVENTION:
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                                                  Difiore,
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Francesca
A Substrate for the
                                                  Pier P
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%; Pred. No. 0.36;
108; Mismatches 151; Indels
    Epidermal Growth
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US-08-480-145-1/c

Sequence 1, Application US/08480145 Patent No. 5717067

GENERAL INFORMATION:

APPLICANT: Difiore, Pier P APPLICANT: Fazioli, France

APPLICANT: Fazioli, TITLE OF INVENTION: TITLE OF INVENTION:

Francesca A Substrate for the Epidermal Growth Factor Receptor Kinase

CORRESPONDENCE ADDRESS

ADDRESSEE:

E: Knobbe, Martens, Olson & Bear 620 Newport Center Drive, Sixteenth Floor

CITY: Newport Beach STATE: California

COUNTRY:

States of

NUMBER OF SEQUENCES:

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; FEATURE:
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; LOCATION:
US-08-095-737-1
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Best Local Similarity 51.3%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                     1453 acacttgtatttctacataggatgtcgtcatgaaagtccataaaccatccagcggactaa 1512
                          1573 tttcaagaggatatgtttgaaagaaacaaaaaaaaaa 1610
                                                                                              1513 tttcatattaaacattaatgtttccttataatgcattttcatgaaatctctattgtgaca 1572
                                                                                                                                 3840 ACAATTTTATAGGTGAAAAACATGAAGTGAGTAAATAAACTAAACCACAAAGATGGACAA 3781
3720 TTTCAAGTAAATGAGCCTTCATTAAAAAAAAAAAAAAACA
                                                               3780 AAAGCAATATGATATAAAACACATCACTTTTTCTATTTGTATTCAGTGAAAGTTTTTACA 3721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Factor Receptor Kinase NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL:
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FILING DATE: 19930722
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CLASSIFICATION:
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STATE: California
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3683
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Diffore, Pier P
APPLICANT: Fazioli, Francesca
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                      NUMBER OF SEQUENCES: 4
                                                                                                                                                                                     ITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 51.38;
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 OPERATING SYSTEM:
                 COMPUTER:
                                                                                                             CITY:
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California
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compatible
PC-DOS/MS-DOS
                                                                                                                                                                                 A Substrate for the Epidermal Growth Factor Receptor Kinase
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Pred. No. 1.9;
                                                                                                                          Drive, Sixteenth Floor
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                                                                ; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-27
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Matches
                                                                                                                                SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                      APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna
                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/00
APPLICATION 2-JUL-1993
                                                                                                                 LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1573 tttcaagaggatatgtttgaaagaaacaaaaaaaaaaa 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3780 AAAGCAATATGATATAAAACACATCACTTTTTCTATTTGTATTCAGTGAAAGTTTTTACA 372:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1513 tttcatattaaacattaatgtttccttataatgcattttcatgaaatctctattgtgaca 1572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: NIH060.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/477,389 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   27, Application US/09188930A
o. 6150502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 2.2%;
l Similarity 51.3%;
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                FastSEQ
                                                                                                                                                                                                                                                                                               Strachan, Lorna
Sleeman, Matthew
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21..2709
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                                                                                                                                                  for Windows Version 3.0
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235-0176
2.1%;
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Pred. No. 1.9;
0; Mismatches
Score 34; DB 3; Pred. No. 1.3;
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               Length 778;
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DB 6;

Length 5177;

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5352450-1
                                                                                                                                           PATENT NO. 5352450

APPLICANT: KOGA, TOSHIHIKO;OKAHASHI, NOBUO;TAKAHASHI, ICHIRO;
SHIBUYA, KOJI;OHTA, HIROTAKA
TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL
                                                                                                                                                                                                                            5352450-1
                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rat
US-09-188-930-202
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                                 SEQ ID NO:1
                                                                                                                                  CARIES AND VACCINAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 202
LENGTH: 778
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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                              NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    122 aatgaaatggaaaacatttattacacaaatttaattacaattctag 167
                                                                                                                                                                                                                                                                                                                       922 actagcaaagcaatattaaaattacacgaaatactttggagttccag 967
                                                                                                                                                                                                                                                                                                                                                                              863 aattgattootgaacaagcattgataggtgca-gtttatcatccaattttotgcctotgaa 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                    803 tygaaaacyctaatayyytaaacaaayayctayctyctyataccctayattttcttcata 862
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                                             APPLICATION NUMBER: US/
FILING DATE: 29-MAY-1990
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5177
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                                                                                                                                COMPOSITIONS FOR DENTAL CARIES USED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%;
                                                              US/07/529,602
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Pred. No. 1.3;
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Best Local Similarity
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US-08-742-185-101/c
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                                                  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/C
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 MOLECULE TYPE:
                                                                                                                                                TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                           FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 00
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      729 atgaaaaagatatggcagctcataaagccgaggttgaacgcattaatgctgcaaatgctg 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                   STRANDEDNESS:
                       TOPOLOGY:
                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagttccagatgttccccgtcctattggaaaccgcaga 996
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                                                                                                                                                                                                                     Granahan, Patric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two Militia Drive
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                       linear
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DNA (genomic)
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Pred. No. 3
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Matches 10
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                Query Match
Best Local Similarity
   Matches
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                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/133,390
FILING DATE: 08-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                nucleic acid
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3000 K Street, N.W.,
ashington, D.C.
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NILSSON, Dan
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               Score 33:4; DI
Pred. No. 2.7;
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Best Local Similarity
Matches 113; Conserv
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 885 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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KATO, IKUNOSHIN
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Pred. No. 2
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Best Local Similarity

Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
827 TGTAAC 832
                          660 agcaac 665
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CORRESPONDENCE ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, STREET: PO BOX 747
                                                                                                                                                                    587
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1588 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: PO BOA / , CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                              POPOLOGY:
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                                              tcctgtttataaatttagtaattttatcggacagttggagagcagaatttcccaaggcgc 659
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KATO, IKUNOSHIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,16
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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2182 TGTAAC 2187
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TYPE: nucleic acid
STRANDEDESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genom:
                                                                                                            2002 CAATGTAATCAATAATACAGTTGAAAAAGGAGATTATTTAATATCCTCATCAAATATTGC 2061
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LENGTH: 4146 base pair
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                            660 agcaac 665
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ADDRESSEE: BIRCH, ST
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APPLICANT: UENO, HARUMI
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                             AL108721 Drosophil
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AL167541 Tetraodon
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                             source
                          genome. For more into: //www.genoscope.cns.fr/Tetraodon.http://www.genoscope.cns.fr/Tetraodon.bcation/Qualifiers
                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 819)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROUSEST-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, Weissenbach, J.
                                                                                                                                                                                          Genoscope.
Direct Sub
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                                                                                                                                                                                                                                                          Unpublished
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Roest-Crollius, H.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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                                                                                                    genome. For more information, please 
http://www.genoscope.cns.fr/Tetraodon
                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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/organism="Tetraodon nigroviridis"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWAHWWA 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome sum BACR08K10 of RPCI-98 library from
                                                                                  and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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151 c 137 g 327 t 118 others
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/organism="Drosophila melanogaster"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the European Drosophila
                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                        Direct Submission
                                                                                                          Genoscope
                                                                                                                                                                                                                                                                                    CNS0107S 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03C18 of DrosBAC library from Drosophila melanogaster (fruit
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                                             - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Unacomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence BACN06G12 of DrosBAC library from Drosophila me
                                           pBeloBAC11
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                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
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/clone="BACN03C18"
/note="end : SP6"
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Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                            Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37F07 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly), genomic survey sequence.
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